

From: Pak, Yong  
Sent: Tuesday, January 15, 2002 1:38 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/654,652

dear stic,

please search the following in commercial and interference database for 09/654,652:

1. SEQ ID NO:3
2. oligomer search of SEQ ID NO:3

Yong Pak

Art Unit 1652  
CM1 10A16 (mail box 10C01)  
703-308-9363

Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, .rapm and .rapn

***The Pending database search results should not be left in the case because they contain data that is confidential.***

Searcher: P. Nelson - Early  
Phone: 308-4501  
Location: Biotech Lib.  
Date Picked Up: 1/15/02  
Date Completed: 1/15/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: 5m  
Online time: 4m

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: ABSS02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 15, 2002, 15:48:20 ; Search time 12.57 Seconds

(without alignments)  
624.793 Million cell updates/sec

Title: US-09-654-652A-3

Perfect score: 1824

Sequence: 1 MNIKKTAVKSALAVAAAAA.....AKGAKVNPNGHKRYRVNFEH 349

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/CTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210	66.3	228	3	US-09-286-690-12 Sequence 12, App1
2	248	13.6	239	1	US-08-103-998-2 Sequence 2, App1
3	248	13.6	242	3	US-09-286-690-8 Sequence 8, App1
4	233.5	12.8	243	3	US-09-286-690-10 Sequence 10, App1
5	231.5	12.7	279	3	US-09-286-690-9 Sequence 9, App1
6	227.5	12.5	238	3	US-09-286-690-7 Sequence 7, App1
7	224.5	12.3	242	3	US-09-286-690-11 Sequence 11, App1
8	222.5	12.2	237	1	US-08-103-998-4 Sequence 4, App1
9	190.5	10.4	245	3	US-09-286-690-2 Sequence 2, App1
10	159.5	8.7	306	2	US-08-824-707-2 Sequence 2, App1
11	145	7.9	263	4	US-09-159-106-2 Sequence 2, App1
12	144	7.9	435	4	US-09-159-106-11 Sequence 11, App1
13	141.5	7.8	303	4	US-09-159-106-13 Sequence 13, App1
14	133.5	7.3	276	2	US-08-712-072C-4 Sequence 4, App1
15	119	6.5	321	2	US-08-712-072C-3 Sequence 3, App1
16	117.5	6.4	289	2	US-08-580-545B-4 Sequence 4, App1
17	117.5	6.4	289	4	US-09-262-653A-4 Sequence 4, App1
18	117.5	6.4	289	4	US-08-867-484A-2 Sequence 2, App1
19	116.5	6.4	654	1	US-08-392-828C-2 Sequence 2, App1
20	116.5	6.4	654	3	US-09-330-945-2 Sequence 2, App1
21	115	6.3	262	1	US-08-392-828C-37 Sequence 37, App1
22	115	6.3	262	3	US-09-330-945-37 Sequence 37, App1
23	113	6.2	285	2	US-08-712-072C-5 Sequence 5, App1
24	110.5	6.1	295	1	US-08-295-657-3 Sequence 3, App1
25	110	6.0	287	4	US-08-640-737-8 Sequence 8, App1
26	109.5	6.0	289	4	US-08-640-737-2 Sequence 2, App1
27	107.5	5.9	666	4	US-08-961-083-2 Sequence 2, App1

28	106.5	5.8	682	3	US-08-481-435-6 Sequence 6, App1
29	105	5.8	422	2	US-08-712-072C-2 Sequence 2, App1
30	104	5.7	348	4	US-09-216-295-16 Sequence 16, App1
31	103.5	5.7	395	2	US-08-404-531B-3 Sequence 3, App1
32	103.5	5.7	395	3	US-08-476-900A-3 Sequence 3, App1
33	103.5	5.7	395	3	US-08-488-546A-3 Sequence 3, App1
34	103.5	5.7	1580	4	US-08-726-320-1 Sequence 1, App1
35	103.5	5.7	1580	4	US-09-208-716-1 Sequence 1, App1
36	103.5	5.7	1581	4	US-08-726-320-3 Sequence 3, App1
37	103.5	5.7	1581	4	US-09-208-716-3 Sequence 3, App1
38	98.5	5.4	1581	2	US-08-404-531B-6 Sequence 6, App1
39	98.5	5.4	1581	3	US-08-476-900A-6 Sequence 6, App1
40	98.5	5.4	1581	3	US-08-488-546A-6 Sequence 6, App1
41	97.5	5.3	1385	1	US-07-876-280-2 Sequence 2, App1
42	97.5	5.3	1385	1	US-07-875-772-2 Sequence 2, App1
43	97.5	5.3	1385	1	US-08-053-170-2 Sequence 2, App1
44	97.5	5.3	1385	1	US-08-158-232-2 Sequence 2, App1
45	97.5	5.3	1385	1	US-08-304-626-2 Sequence 2, App1

## ALIGNMENTS

RESULT 1  
US-09-286-690-12  
; Sequence 12, Application US/09286690  
; Patent No. 6103511  
; GENERAL INFORMATION:  
; APPLICANT: Li, Xin-Liang  
; APPLICANT: Ljunggahl, Lars G.  
; APPLICANT: Chen, Huizhong  
; TITLE OF INVENTION: Lichenase and Coding Sequences  
; FILE REFERENCE: 55-96  
; CURRENT APPLICATION NUMBER: US/09/286, 690  
; CURRENT FILING DATE: 1999-04-05  
; EARLIER APPLICATION NUMBER: US 60/027, 882  
; EARLIER FILING DATE: 1999-10-04  
; EARLIER APPLICATION NUMBER: PCT/US97/17811  
; EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Fibrobacter succinogenes  
US-09-286-690-12

Query Match 66.3%; Score 1210; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 8.4e-103;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNIKKTAVKSALAVAAAAAATTNWSAKDFSGAFLYLLEEVYQKFEARKMAASTVS 60  
DB 1 MNIKKTAVKSALAVAAAAAATTNWSAKDFSGAFLYLLEEVYQKFEARKMAASTVS 60  
QY 61 SMFLYQNGSEIADRPVPEVDIEVLGNPSPFOSNITTKRGAOKTSEKHAAVSPADQA 120  
DB 61 SMFLYQNGSEIADRPVPEVDIEVLGNPSPFOSNITTKRGAOKTSEKHAAVSPADQA 120  
QY 121 FHVYGLFMTNRYVWTVDSGEVRRKTEGGVSNLTGTGRLRNLMSSSSAAMVGGFDESKL 180  
DB 121 FHVYGLFMTNRYVWTVDSGEVRRKTEGGVSNLTGTGRLRNLMSSSSAAMVGGFDESKL 180  
QY 181 PLEQFIMVWVYKVTTPGQGGSGFTLDWTDNPTTPFGSRWKGKDWTF 228  
DB 181 PLEQFIMVWVYKVTTPGQGGSGFTLDWTDNPTTPFGSRWKGKDWTF 228  
RESULT 2  
US-08-103-998-2  
; Sequence 2, Application US/08103998  
; Patent No. 5470725

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Query Match          13.6%: Score 248; DB 1; Length 239;  
Best Local Similarity   35.4%; Pred. No. 5.2e-15;  
Matches      627; Conservative    27; Mismatches    70; Indels    16; Gaps    8  
  
OY      23 TNNVSAKDPSGAEVLTELVQYGKFAFRKKMAAASGVSSMFLYONCSELTADGRPWVEVDI 82  
       | : | : | : | : | : | : | : | : | : | : | : | : |  
Db      77 TSPTSNRKDCCEBNSVSQTGYTGLEVRKRPAKNITIVSFFPYTGPTE---CTPMDEIDI 133  
  
OY      83 EVLGNPESFOSNITTGKAGAKOIKSEKHHAAPRADOAFHTYTGLEMTFYVHWTVDGGEV 142  
       ||||| : | : | : | : | : | : | : | : | : | : | : | : |  
Db     134 EFLCKDTTKKYVPNTTYNGVGCH--EKVISLGFDMSKGHRTIAFMORQETIMNYDGG-VL 189  
  
OY      143 RKTEGCQGVSNLTGTQG-LRFNMISSES-AWVGOFDESRLPLFOFINMKVKYYKT 195  
       : | : | : | : | : | : | : | : | : | : | : | : |  
Db     190 KHT---ATANIPSTPGKIMNMILMNCGTDGMDSINGAN-PLYAEIDMV---KYT 237  
  
RESULT        3  
US-09-286-690-8  
Sequence 8, Application US/09286690  
Patent No. 6103511  
GENERAL INFORMATION:  
APPLICANT: Li, Xin-Liang  
APPLICANT: Ljungdahl, Lars G.  
TITLE OF INVENTION: Lichenase and Coding Sequences  
FILE REFERENCE: 55-96  
CURRENT APPLICATION NUMBER: US/09/286,690  
CURRENT FILING DATE: 1999-04-05
```

Query Match	13.6%	Score 248	DB 3	length 242
Best Local Similarity	36.0%	Pred. No. 5.3e-15		
Matches	63	Conservative	25	Mismatches 75
				Indels 12
				Gaps 7

RESULT 4  
US-09-286-690-10  
: Sequence 10, Application US/09286650

Query March	12.8%	Score 233.5	DB 3	Length 243
Best Local Similarity	33.7%	Pred. No. 1.1e-13		
Matches 58; Conservative	26;	Mismatches 77;	Indels 11;	Gaps 6;

RESULT	5
Qy	23 TWSAKFSGSGLTLEEVQYKGEAREKRMMAASGTWSMFLYQNGSEIADGRPVEVDI 82
Db	81 TSPSYNKFDCGNSSVQTYGYGLAEVNMRKPAKNNGVGSFFTYTQPT---DGTWDELDI 137
Qy	83 EVLGKMGSGFOSNIITGKAGAKQKTSSEKIHAVSPAADQAFHTYTGLEMTPTNYVRWYDGEV 142
Db	138 EFLCKDPTTKVQENFYTYTNGVG---NHEKLVNIGFPAANSTHTYAFDMDQNSISIKWYDQ-L 193
Qy	143 RKTGGGVSNLTQGLRFLNLSSESA-AWVGQFDESKLPTFOFINWVKYK 193
Db	194 KHTATTTDIPQPKK-LMMNLMNGAGVDWGLGSYN-GVTPFLSRSLHWRYRYIK 242



COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/103,998  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/773,652  
FILING DATE: 16-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30307/123  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 237 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-103-998-4

Query Match 12.2%; Score 222.5; DB 1; Length 237;  
Best Local Similarity 33.1%; Pred. No. 1.1e-12;  
Matches 57; Conservative 25; Mismatches 79; Indels 11; Gaps 6;  
QY 23 TNSAKDFSGAELTYLEVOYGFEPARKMAAASGVSSMFLYQNGSEIADGRPWVEV 82  
DB 75 TSSAYNKFDCAEYRSTNYIGVLEYSMKPAKNTGIVSSFFTYTGP---AHGTQDEIDI 131  
QY 83 EVIGKNPSPQSNITTGKAGAKTSEKHNAVSPADQAFHTYGLTMTNPNVYVWTVDGQEV 142  
DB 132 EFLGADTTKKVQFNYYTNGAG--NHKEFADLGFEDANAYHTYAFWQPSIKWYDGO-L 187  
QY 143 RKTGGQVSNLTGTGGLRFLNLSSESA-AWVGQFDESKLPLFQFTINWYKVK 193  
DB 188 KHTATGTIPAPBK--IMMNLNMGVGDWDLGSYGVN-PIVAHDMWRK 236

RESULT 9  
US-09-286-690-2  
Sequence 2, Application US/05286690  
Patent No. 6103511  
GENERAL INFORMATION:  
APPLICANT: Li, Xin-Liang  
APPLICANT: Ljungdahl, Lars G.  
APPLICANT: Chen, Huizhong  
TITLE OF INVENTION: Lichenase and Coding sequences  
FILE REFERENCE: 55-96  
CURRENT APPLICATION NUMBER: US/09/286,690  
EARLIER FILING DATE: 1999-04-05  
EARLIER APPLICATION NUMBER: US 60/027,882  
EARLIER FILING DATE: 1999-10-04  
EARLIER APPLICATION NUMBER: PCT/US97/17811  
EARLIER FILING DATE: 1997-10-03  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Orpiniomyces sp. PC-2  
US-09-286-690-2

Query Match 10.4%; Score 190.5; DB 3; Length 245;  
Best Local Similarity 31.6%; Pred. No. 9.6e-10;  
Matches 54; Conservative 17; Mismatches 87; Indels 13; Gaps 6;  
QY 21 LTTNSAKDFSGAELTYLEVOYGFEPARKMAAASGVSSMFLYQNGSEIADGRPWVEV 80  
DB 79 LTIDDGSGYTCGEYRFTNYYGGMFQVNMKPKNPQVSSFFTYTGPS---DGTKMDEI 135  
QY 81 DIEVLGKNPSPQSNITTGKAGAKTSEKHNAVSPADQAFHTYGLTMTNPNVYVWTVDGQ 140  
DB 136 DIEFLGYPTTKVQFNYYTNGAGH--EHIHLGDSAGQFHTYGFPAKNSITMYVGT 192  
QY 141 EVRKTGGQVSNLTGTGGLRFLNLSSESA-AWVGQFDESKLPLFQFTINW 189  
DB 193 AVYTA---YDNIPTPKIMMNAWNGVGDWDLRPFN-GRINISAYYDWV 238

RESULT 10  
US-08-824-707-2  
Sequence 2, Application US/08824707  
Patent No. 5919688  
GENERAL INFORMATION:  
APPLICANT: Ferrier, Pau  
APPLICANT: Diers, Ivan  
APPLICANT: Hedegaard, Lisbeth  
APPLICANT: Halkier, Torben  
APPLICANT: Asejo, Juan  
APPLICANT: Sava, Demitris  
TITLE OF INVENTION: No. 5919688e1 enzyme with beta-1,3-glucanase activity  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 59196880 No. 5919688e1 of No. 5919688th America, Inc.  
STREET: 405 Lexington Avenue, Suite 6400  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/824,707  
FILING DATE: 14-April-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Gregg, Valeta A.  
REGISTRATION NUMBER: 35,127  
REFERENCE/DOCKET NUMBER: 4290, 204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 306 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-824-707-2

Query Match 8.7%; Score 159.5; DB 2; Length 306;  
Best Local Similarity 27.6%; Pred. No. 9e-07;  
Matches 59; Conservative 29; Mismatches 89; Indels 37; Gaps 11;  
QY 2 NIKTAVKSAALAVAAAAALTTNSAKDFSGAELTYLEEV--QYGFEPARKMAAASGV 59  
DB 103 NYTTSRVNSALDQGNLVTALQESDGSYTSARLTGTQGNVOPQFGRIRARIQIPRGQI 162  
QY 60 SSMFLYQNGSEIADGRPWV---EVDI-EVLGNP-----GSPQSNITTGKAGAKTSEKH 111  
DB 163 SAFWVW--GANLPD--TPWPTSGEIDIMENVGNAPREHVHGVHGPYSGDNGIMTYQHPQ 219



Query Match	7.8%	Score 141.5	DB 4	Length 303
Best Local Similarity	23.0%	Pred. No. 3.9e-05		
Matches	68	Conservative	34	Mismatches 85; Indels 109; Gaps 15
OY	6	TAWSALAVAAAAALT	--TNVSA-----KPFSGA-----	33
	:	:	:	
DB	28	SALVAAALTRAAALAVTAATSAARPDLLMSDEDFGAGSAPNPAYVNHHTGAHGKN		87
OY	34	--EUYTLE-----	-----EYVYKGFPAKMAAA	55
	:	:	:	
DB	88	AELOWYTSRANSALDGGCNLTARREGDSYTSARMTQCKYQPYQVIGEARIQIDPRG		147
OY	56	SGTWSMELYONGSEIADGRPVY---EVDI-EVLKNP---GSFOSNITTKAGAOKTS		107
	:	:	:	
DB	148	QG-IMPAPMLGGS--FGTPWPSGSEIDIMENYGFEPHRYHGVTHGPGYSGSGT--TG		202
OY	108	EKNHNVSRADDAFTTUGLEMTFRNVKRYTVDSQEVYKTKEGGOYSLTGTQGLRFLMSE		167
	:	:	:	
DB	203	MYHNGQMSFADTFHTGFVDMKRFEGITGFVDDQDQHNRYTRASVG-----		246
OY	168	SAAMVSGDESKLRYLRFQFLNMYKKVKKYRSGOEGSS---DFTLLMDNDFDFFDS		219
	:	:	:	
DB	247	ANAWY--EDQ---REFLLTN-VAAGGQWKGPRDGTQTLRQOKKUYUVRVYVDDGSS		296



